James G Wilson

List of Publications by Citations

535 papers	81,755 citations	132 h-index	280 g-index
602 ext. papers	104,523 ext. citations	14.3 avg, IF	6.36 L-index

#	Paper	IF	Citations
535	Analysis of protein-coding genetic variation in 60,706 humans. *Nature*, **2016**, 536, 285-91	50.4	6940
534	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
533	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
532	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
531	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
530	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
529	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
528	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
527	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
526	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
525	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
524	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
523	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. *Nature Genetics*, **2018**, 50, 1112-1121	36.3	950
522	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
521	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
520	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. *Nature Genetics*, **2012**, 44, 491-501	36.3	866
519	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850

518	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
517	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
516	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
515	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. *Nature Genetics*, **2009**, 41, 47-55	36.3	708
514	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
513	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. *Lancet, The*, **2012**, 379, 1214-24	40	658
512	An epigenetic biomarker of aging for lifespan and healthspan. *Aging*, **2018**, 10, 573-591	5.6	658
511	Runs of homozygosity in European populations. *American Journal of Human Genetics*, **2008**, 83, 359-72	11	624
510	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
509	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
508	New loci associated with kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 376-84	36.3	599
507	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
506	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
505	SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. *Nature Genetics*, **2008**, 40, 437-42	36.3	563
504	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
503	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
502	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. *Lancet, The*, **2012**, 379, 1205-13	40	522
501	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. *Nature Genetics*, **2010**, 42, 436-40	36.3	521

500	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
499	Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations. *PLoS Genetics*, **2009**, 5, e1000504	6	495
498	A genetic atlas of human admixture history. *Science*, **2014**, 343, 747-751	33.3	492
497	Genomic insights into the origin of farming in the ancient Near East. *Nature*, **2016**, 536, 419-24	50.4	485
496	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463
495	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. *Journal of the American College of Cardiology*, **2016**, 67, 2578-89	15.1	458
494	Genetic mechanisms of critical illness in COVID-19. *Nature*, **2021**, 591, 92-98	50.4	451
493	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
492	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430
491	DNA methylation GrimAge strongly predicts lifespan and healthspan. *Aging*, **2019**, 11, 303-327	5.6	424
490	Mendelian randomization of blood lipids for coronary heart disease. *European Heart Journal*, **2015**, 36, 539-50	9.5	417
489	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
488	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. *Lancet, The*, **2015**, 385, 351-61	40	409
487	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
486	Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. *Circulation*, **2011**, 123, 731-8	16.7	395
485	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
484	A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genetics*, **2014**, 10, e1004234	6	377
483	Abundant pleiotropy in human complex diseases and traits. *American Journal of Human Genetics*, **2011**, 89, 607-18	11	376

482	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. *Nature Genetics*, **2010**, 42, 1077-85	36.3	372
481	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
480	Population genetic structure of variable drug response. *Nature Genetics*, **2001**, 29, 265-9	36.3	344
479	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
478	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607	6	326
477	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
476	High throughput isolation and glycosylation analysis of IgG-variability and heritability of the IgG glycome in three isolated human populations. *Molecular and Cellular Proteomics*, **2011**, 10, M111.010090	7.6	324
475	Concept, design and implementation of a cardiovascular gene-centric 50 k SNP array for large-scale genomic association studies. *PLoS ONE*, **2008**, 3, e3583	3.7	321
474	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. *Nature Genetics*, **2013**, 45, 314-8	36.3	314
473	Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
472	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313
471	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
470	Inactivating mutations in NPC1L1 and protection from coronary heart disease. *New England Journal of Medicine*, **2014**, 371, 2072-82	59.2	307
469	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
468	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
467	Genomic runs of homozygosity record population history and consanguinity. *PLoS ONE*, **2010**, 5, e13996	3.7	281
466	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
465	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268

464	Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. *Science Translational Medicine*, **2015**, 7, 270ra6	17.5	267
463	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	32.4	266
462	Novel associations of multiple genetic loci with plasma levels of factor VII, factor VIII, and von Willebrand factor: The CHARGE (Cohorts for Heart and Aging Research in Genome Epidemiology) Consortium. *Circulation*, **2010**, 121, 1382-92	16.7	260
461	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. *Nature Genetics*, **2019**, 51, 245-257	36.3	259
460	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
459	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
458	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
457	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2014**, 2, 719-29	18.1	250
456	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
455	Genome-wide association study of coronary heart disease and its risk factors in 8,090 African Americans: the NHLBI CARe Project. *PLoS Genetics*, **2011**, 7, e1001300	6	249
454	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. *Nature Genetics*, **2012**, 44, 260-8	36.3	243
453	The landscape of recombination in African Americans. *Nature*, **2011**, 476, 170-5	50.4	243
452	Loci associated with N-glycosylation of human immunoglobulin G show pleiotropy with autoimmune diseases and haematological cancers. *PLoS Genetics*, **2013**, 9, e1003225	6	242
451	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
450	Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. *American Journal of Human Genetics*, **2014**, 94, 223-32	11	233
449	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. *Nature Genetics*, **2013**, 45, 76-82	36.3	232
448	Runs of homozygosity: windows into population history and trait architecture. *Nature Reviews Genetics*, **2018**, 19, 220-234	30.1	231
447	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226

446	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. *PLoS Medicine*, **2017**, 14, e1002383	11.6	223
445	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. *JAMA Psychiatry*, **2015**, 72, 642-50	14.5	222
444	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. *Nature Genetics*, **2013**, 45, 155-63	36.3	222
443	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. *PLoS Genetics*, **2016**, 12, e1006125	6	222
442	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
441	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
440	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
439	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
438	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. *American Journal of Human Genetics*, **2012**, 90, 410-25	11	214
437	Best practices and joint calling of the HumanExome BeadChip: the CHARGE Consortium. *PLoS ONE*, **2013**, 8, e68095	3.7	203
436	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
435	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
434	Glycans are a novel biomarker of chronological and biological ages. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2014**, 69, 779-89	6.4	192
433	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
432	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and studies. *Aging*, **2018**, 10, 1758-1775	5.6	187
431	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
430	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. *Nature Genetics*, **2010**, 42, 430-5	36.3	184
429	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181

428	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
427	Positive selection on a high-sensitivity allele of the human bitter-taste receptor TAS2R16. *Current Biology*, **2005**, 15, 1257-65	6.3	180
426	Genomics meets glycomics-the first GWAS study of human N-Glycome identifies HNF1 as a master regulator of plasma protein fucosylation. *PLoS Genetics*, **2010**, 6, e1001256	6	177
425	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. *Nature Communications*, **2018**, 9, 260	17.4	174
424	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. *Nature Genetics*, **2014**, 46, 1126-1130	36.3	171
423	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. *Nature Genetics*, **2017**, 49, 416-425	36.3	170
422	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
421	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. *Nature Genetics*, **2011**, 43, 940-7	36.3	168
420	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PLoS Genetics*, **2012**, 8, e1002741	6	162
419	Genetic evidence for different male and female roles during cultural transitions in the British Isles. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 5078-83	11.5	157
418	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. *Nature Genetics*, **2019**, 51, 481-493	36.3	156
417	Causal effects of body mass index on cardiometabolic traits and events: a Mendelian randomization analysis. *American Journal of Human Genetics*, **2014**, 94, 198-208	11	156
416	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. *Nature Genetics*, **2019**, 51, 30-35	36.3	153
415	Meta-analysis of genome-wide association studies in African Americans provides insights into the genetic architecture of type 2 diabetes. *PLoS Genetics*, **2014**, 10, e1004517	6	151
414	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. *American Journal of Human Genetics*, **2018**, 103, 691-706	11	151
413	Genetic determinants of circulating sphingolipid concentrations in European populations. *PLoS Genetics*, **2009**, 5, e1000672	6	150
412	Admixture mapping of white cell count: genetic locus responsible for lower white blood cell count in the Health ABC and Jackson Heart studies. *American Journal of Human Genetics*, **2008**, 82, 81-7	11	150
411	Genetic adaptation of fatty-acid metabolism: a human-specific haplotype increasing the biosynthesis of long-chain omega-3 and omega-6 fatty acids. *American Journal of Human Genetics*, **2012**, 90, 809-20	11	148

410	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
409	Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations. *PLoS Genetics*, **2012**, 8, e1002490	6	145
408	Y chromosomes traveling south: the cohen modal haplotype and the origins of the Lemba--the "Black Jews of Southern Africa". *American Journal of Human Genetics*, **2000**, 66, 674-86	11	144
407	Genome-wide association and functional follow-up reveals new loci for kidney function. *PLoS Genetics*, **2012**, 8, e1002584	6	143
406	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
405	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. *Nature Genetics*, **2018**, 50, 834-848	36.3	135
404	A predominantly indigenous paternal heritage for the Austronesian-speaking peoples of insular Southeast Asia and Oceania. *American Journal of Human Genetics*, **2001**, 68, 432-43	11	134
403	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
402	A Y chromosome census of the British Isles. *Current Biology*, **2003**, 13, 979-84	6.3	129
401	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
400	Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. *Journal of the American College of Cardiology*, **2016**, 68, 2761-2772	15.1	127
399	Association of sickle cell trait with chronic kidney disease and albuminuria in African Americans. *JAMA - Journal of the American Medical Association*, **2014**, 312, 2115-25	27.4	126
398	Candidate gene association resource (CARe): design, methods, and proof of concept. *Circulation: Cardiovascular Genetics*, **2010**, 3, 267-75		125
397	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. *Human Molecular Genetics*, **2010**, 19, 4304-11	5.6	125
396	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
395	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. *Behavior Genetics*, **2016**, 46, 170-82	3.2	122
394	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
393	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. *American Journal of Human Genetics*, **2018**, 102, 88-102	11	119

392	Nine loci for ocular axial length identified through genome-wide association studies, including shared loci with refractive error. *American Journal of Human Genetics*, **2013**, 93, 264-77	11	116
391	Founding mothers of Jewish communities: geographically separated Jewish groups were independently founded by very few female ancestors. *American Journal of Human Genetics*, **2002**, 70, 1411-20	11	113
390	Genome-wide association study of white blood cell count in 16,388 African Americans: the continental origins and genetic epidemiology network (COGENT). *PLoS Genetics*, **2011**, 7, e1002108	6	111
389	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. *JAMA - Journal of the American Medical Association*, **2017**, 317, 937-946	27.4	109
388	Multiethnic meta-analysis of genome-wide association studies in >100 000 subjects identifies 23 fibrinogen-associated Loci but no strong evidence of a causal association between circulating fibrinogen and cardiovascular disease. *Circulation*, **2013**, 128, 1310-24	16.7	107
387	Genome-wide association analysis identifies multiple loci related to resting heart rate. *Human Molecular Genetics*, **2010**, 19, 3885-94	5.6	106
386	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
385	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
384	Assessing the phenotypic effects in the general population of rare variants in genes for a dominant Mendelian form of diabetes. *Nature Genetics*, **2013**, 45, 1380-5	36.3	103
383	Imputation of exome sequence variants into population- based samples and blood-cell-trait-associated loci in African Americans: NHLBI GO Exome Sequencing Project. *American Journal of Human Genetics*, **2012**, 91, 794-808	11	103
382	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
381	A combined long-range phasing and long haplotype imputation method to impute phase for SNP genotypes. *Genetics Selection Evolution*, **2011**, 43, 12	4.9	101
380	Meta-analysis of genome-wide association studies identifies six new Loci for serum calcium concentrations. *PLoS Genetics*, **2013**, 9, e1003796	6	100
379	Genome-wide association uncovers shared genetic effects among personality traits and mood states. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 684-95	3.5	98
378	Extensive female-mediated gene flow from sub-Saharan Africa into near eastern Arab populations. *American Journal of Human Genetics*, **2003**, 72, 1058-64	11	97
377	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. *Cell*, **2017**, 170, 199-212.e20	56.2	94
376	Multiple loci are associated with white blood cell phenotypes. *PLoS Genetics*, **2011**, 7, e1002113	6	92
375	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. *Nature Communications*, **2016**, 7, 12522	17.4	90

374	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
373	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. *Nature Communications*, **2018**, 9, 3391	17.4	90
372	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. *PLoS Genetics*, **2019**, 15, e1008500	6	90
371	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
370	Chronotype and sleep duration: the influence of season of assessment. *Chronobiology International*, **2014**, 31, 731-40	3.6	87
369	Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARe and a Breast Cancer Consortium. *PLoS Genetics*, **2011**, 7, e1001371	6	86
368	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. *Genome Medicine*, **2017**, 9, 23	14.4	85
367	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
366	Plasma phosphatidylcholine and sphingomyelin concentrations are associated with depression and anxiety symptoms in a Dutch family-based lipidomics study. *Journal of Psychiatric Research*, **2013**, 47, 357-62	5.2	84
365	Association between chromosome 9p21 variants and the ankle-brachial index identified by a meta-analysis of 21 genome-wide association studies. *Circulation: Cardiovascular Genetics*, **2012**, 5, 100-12		84
364	A meta-analysis and genome-wide association study of platelet count and mean platelet volume in african americans. *PLoS Genetics*, **2012**, 8, e1002491	6	84
363	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. *ELife*, **2019**, 8,	8.9	82
362	Association of Sickle Cell Trait With Hemoglobin A1c in African Americans. *JAMA - Journal of the American Medical Association*, **2017**, 317, 507-515	27.4	81
361	Pleiotropic genes for metabolic syndrome and inflammation. *Molecular Genetics and Metabolism*, **2014**, 112, 317-38	3.7	81
360	Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. *Human Molecular Genetics*, **2009**, 18, 373-80	5.6	81
359	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics. *Human Molecular Genetics*, **2017**, 26, 438-453	5.6	80
358	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. *Nature Genetics*, **2017**, 49, 125-130	36.3	80
357	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. *Behavior Genetics*, **2014**, 44, 295-313	3.2	80

356	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. *Nature Communications*, **2016**, 7, 11008	17.4	79
355	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
354	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. *Nature Communications*, **2017**, 8, 910	17.4	78
353	Study design for genetic analysis in the Jackson Heart Study. *Ethnicity and Disease*, **2005**, 15, S6-30-37	1.8	77
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34	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
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1	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		